

Sequence Listing

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Foerderung der
Wissenschaften e.V
- (B) STREET: none
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE: none

(ii) TITLE OF INVENTION: Process for increasing the yield in plants

(iii) NUMBER OF SEQUENCES: 1

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) ORIGINAL SOURCE:

- (A) ORGANISM: Agrobacterium rhizogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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AATTCGATAC GAAAAAGGCA AGTGCCAGGG CCATTTAAAA TACGGCGTCG GAAACTGGCG      60
CCAATCAGAC ACAGTCTCTG GTCGGGAAAG CCAGAGGTAG TTTGGCAACA ATCACAACAA      120
GATCGATGCG CAAGACACGG GAGGCCTTAA AATCTGGATC AAGCGAAAAT ACTGCATGCG      180
TGATCGTTCA TGGGTTTATA GTACTGGGTT TGCTTTTCTT TGTCTGTTG TTTGGCCTTA      240
GGGAAAGGAT GTCAAAAAAG GATGCCATA ATTGGGAGGA GTGGGGTAAA GCTTAAAGTT      300
GGCCCCGTAT TGGATTTTGC GAAAGCGGCA TTGGCAAACG TGAAGATTGC TGCAATCAAG      360
ATACTTTTTC TATTTTCTGG TTAAGATGTA AAGTATTGCC ACAATCATAT TAATTACTAA      420
CATTGTATAT GTAATATAST GCGGAAATTA TGTATGCCAA AATGATGTAT TAATAATAGC      480

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AATAATAATA TGTGTTAATC TTTTCAATC GGAATACGT TTAAGCGATT ATCGTGTGA	540
ATAAATTATT CCAAAAGGAA ATACATGTTT TTGGAGAACC TGCTATAGAT ATATGCCAAA	560
TTTACACTAG TTTASTGSGT GCAAAACTAT TATCTCTGTT TCTGAGTTTA ATAAAAATA	580
AATAAGCAGG GCGAATAGCA GTTAGCCTAA GAAGGAATGG TGGCCATGTA CGTGCTTTTA	600
AGAGACCCTA TAATAAATTG CCAGCTGTGT TGCTTTGGTG CCGACAGGCC TAACGTGGGG	620
TTTAGCTTGA CAAAGTAGCG CTTTTCCGCA GCATAAATAA AGGTAGGCGG GTGCGTCCCA	640
TTATTAAAGG AAAAAGCAAA AGCTGAGATT CCATAGACCA CAAACCACCA TTATTGGAGG	660
ACAGAACCTA TTCCCTCAGG TGGGTGGCTA GCTTTAAACC TAATAAGTAA AAACAATTAA	680
AAGCAGGCAG GTGTCCCTTC TATATTGCA CAACGAGGCG ACGTGGAGCA TCGACAGCCG	700
CATCCATTAA TTAATAAATT TGTGGACCTA TACCTAACTC AAATATTTT ATTATTGCT	720
CCAATACGCT AAGAGCTCTG GATTATAAAT AGTTTGGATG CTTCGAGTTA TGGGGTAC	740